

<110> Irei, Reiko  
Tsunoda, Hiroyuki  
Igawa, Tomoyuki  
Sekimori, Yasuo  
Tsuchiya, Masayuki

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Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn  
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Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys	
325 330 335	
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Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met	
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Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg	
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Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp	
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Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser	
485 490 495	
ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc	1536
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser	
500 505 510	
ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca	1584
Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro	
515 520 525	
ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg	1632
Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp	
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Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro  
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Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
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Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
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Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala  
 65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn  
 85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
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Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala  
 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala  
 130 135 140

Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr  
 145 150 155 160

Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser  
 165 170 175

Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr  
 180 185 190

Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser  
 195 200 205

Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His  
 210 215 220  
 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val  
 225 230 235 240  
 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val  
 245 250 255  
 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile  
 260 265 270  
 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu  
 275 280 285  
 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln  
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 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr  
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 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met  
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 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro  
 355 360 365  
 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu  
 370 375 380  
 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg  
 385 390 395 400  
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 405 410 415  
 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp  
 420 425 430  
 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp  
 435 440 445  
 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala  
 450 455 460  
 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu  
 465 470 475 480  
 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser  
 485 490 495  
 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser  
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Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro  
515 520 525

Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp  
530 535 540

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro  
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565 570 575

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1 5 10 15  
ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96  
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30  
gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144  
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser  
35 40 45  
gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192  
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60  
aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240  
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80  
gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288  
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
85 90 95  
ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336  
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
100 105 110  
tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc 384  
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr

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Lys Val Glu Ile Lys Arg Thr	Val Ala Ala Pro Ser Val	Phe Ile Phe	
130	135	140	
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Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys			
145	150	155	160
ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg			528
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val			
165	170	175	
gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag			576
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln			
180	185	190	
gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc			624
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser			
195	200	205	
aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat			672
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His			
210	215	220	
cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt			720
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Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser			
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Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln			
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Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg			
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Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp			
85	90	95	
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr			

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Tyr	Cys	Gln	Gln	Tyr	Tyr	Ser	Thr	Pro	Pro	Thr	Phe	Gly	Gln	Gly	Thr	
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Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	
130					135					140						
Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	
145					150					155					160	
Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	
165					170					175						
Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	
180					185					190						
Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	
195					200					205						
Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	
210					215					220						
Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
225					230					235					240	

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 <213> Homo sapiens  
  
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gct	ggt	cat	gtg	aaa	gcc	caa	gaa	gat	gaa	agg	att	ggt	ctt	ggt	gac	96
Ala	Val	His	Val	Lys	Ala	Gln	Glu	Asp	Glu	Arg	Ile	Val	Leu	Val	Asp	
			20					25					30			
aac	aaa	tgt	aag	tgt	gcc	cgg	att	act	tcc	agg	atc	atc	cgt	tct	tcc	144
Asn	Lys	Cys	Lys	Cys	Ala	Arg	Ile	Thr	Ser	Arg	Ile	Ile	Arg	Ser	Ser	
		35				40					45					
gaa	gat	cct	aat	gag	gac	att	gtg	gag	aga	aac	atc	cga	att	att	ggt	192
Glu	Asp	Pro	Asn	Glu	Asp	Ile	Val	Glu	Arg	Asn	Ile	Arg	Ile	Ile	Val	
	50				55				60							
cct	ctg	aac	aac	agg	gag	aat	atc	tct	gat	ccc	acc	tca	cca	ttg	aga	240
Pro	Leu	Asn	Asn	Arg	Glu	Asn	Ile	Ser	Asp	Pro	Thr	Ser	Pro	Leu	Arg	
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aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat 336  
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 Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg  
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aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc 432  
 Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr  
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<400> 6  
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Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser  
 35 40 45

Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val  
 50 55 60

Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg  
 65 70 75 80

Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro  
 85 90 95

Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn  
 100 105 110

Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg  
 115 120 125

Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr  
 130 135 140

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<210> 18  
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<220>  
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<400> 18  
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<210> 19  
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 <212> DNA  
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<220>  
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 1 5 10 15

gtc cag tgt gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag 96  
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

ccg ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144  
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
 35 40 45

agc agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192  
 Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
 50 55 60

gag tgg gtc tca gct att agt ggt agt ggt tat acc aca tac tac gca 240  
 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala  
 65 70 75 80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac 288  
 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
 85 90 95

acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336  
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
 100 105 110

tat tac tgt gcc aaa aaa ccg ggg gac tat ggt tcg ggg agt tat tac 384

Tyr	Tyr	Cys	Ala	Lys	Lys	Pro	Gly	Asp	Tyr	Gly	Ser	Gly	Ser	Tyr	Tyr	
		115					120					125				
ctt	gac	tac	tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca	ggg	agt	432
Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ser	
	130					135					140					
gca	tcc	gcc	cca	acc	ctt	ttc	ccc	ctc	gtc	tcc	tgt	gag	aat	tcc	ccg	480
Ala	Ser	Ala	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn	Ser	Pro	
145					150					155					160	
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Ser	Asp	Thr	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp	Phe	Leu	
				165				170						175		
ccc	gac	tcc	atc	act	ttc	tcc	tgg	aaa	tac	aag	aac	aac	tct	gac	atc	576
Pro	Asp	Ser	Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser	Asp	Ile	
			180					185					190			
agc	agc	acc	cgg	ggc	ttc	cca	tca	gtc	ctg	aga	ggg	ggc	aag	tac	gca	624
Ser	Ser	Thr	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys	Tyr	Ala	
		195					200				205					
gcc	acc	tca	cag	gtg	ctg	ctg	cct	tcc	aag	gac	gtc	atg	cag	ggc	aca	672
Ala	Thr	Ser	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln	Gly	Thr	
	210					215					220					
gac	gaa	cac	gtg	gtg	tgc	aaa	gtc	cag	cac	ccc	aac	ggc	aac	aaa	gaa	720
Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn	Lys	Glu	
225					230					235					240	
aag	aac	gtg	cct	ctt	cca	gtg	att	gct	gag	ctg	cct	ccc	aaa	gtg	agc	768
Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	
				245					250					255		
gtc	ttc	gtc	cca	ccc	cgc	gac	ggc	ttc	ttc	ggc	aac	ccc	cgc	aag	tcc	816
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	
			260				265					270				
aag	ctc	atc	tgc	cag	gcc	acg	ggt	ttc	agt	ccc	cgg	cag	att	cag	gtg	864
Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	
		275					280					285				
tcc	tgg	ctg	cgc	gag	ggg	aag	cag	gtg	ggg	tct	ggc	gtc	acc	acg	gac	912
Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	
	290					295					300					
cag	gtg	cag	gct	gag	gcc	aaa	gag	tct	ggg	ccc	acg	acc	tac	aag	gtg	960
Gln	Val	Gln	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	
305					310					315					320	
acc	agc	aca	ctg	acc	atc	aaa	gag	agc	gac	tgg	ctc	agc	cag	agc	atg	1008
Thr	Ser	Thr	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Ser	Gln	Ser	Met	
				325					330				335			
ttc	acc	tgc	cgc	gtg	gat	cac	agg	ggc	ctg	acc	ttc	cag	cag	aat	gcg	1056
Phe	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	

340	345	350	
tcc tcc atg tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala 355 360 365			1104
atc ccc cca tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu 370 375 380			1152
acc tgc ctg gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser 385 390 395 400			1200
tgg acc cgc cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser 405 410 415			1248
gag agc cac ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile 420 425 430			1296
tgc gag gat gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr 435 440 445			1344
cac aca gac ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys 450 455 460			1392
ggg gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg 465 470 475 480			1440
gag cag ctg aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr 485 490 495			1488
ggc ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln 500 505 510			1536
ccc ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro 515 520 525			1584
cag gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu 530 535 540			1632
gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu 545 550 555 560			1680
gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly 565 570 575			1728

aaa ccc acc ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc 1776  
Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly  
580 585 590

acc tgc tac tga 1788  
Thr Cys Tyr  
595

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<210> 20
<211> 595
<212> PRT
<213> Homo sapiens
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Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1          5          10          15
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Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln  
20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe  
35 40 45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu  
50 55 60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala  
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn  
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Lys Lys Pro Gly Asp Tyr Gly Ser Gly Ser Tyr Tyr  
115 120 125

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser  
130 135 140

Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro  
145 150 155 160

Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu  
165 170 175

Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile  
180 185 190

Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala  
195 200 205

Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr  
210 215 220

Asp	Glu	His	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn	Lys	Glu	225	230	235	240
Lys	Asn	Val	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	245	250	255	
Val	Phe	Val	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	260	265	270	
Lys	Leu	Ile	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	275	280	285	
Ser	Trp	Leu	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	290	295	300	
Gln	Val	Gln	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	305	310	315	320
Thr	Ser	Thr	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Ser	Gln	Ser	Met	325	330	335	
Phe	Thr	Cys	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	340	345	350	
Ser	Ser	Met	Cys	Val	Pro	Asp	Gln	Asp	Thr	Ala	Ile	Arg	Val	Phe	Ala	355	360	365	
Ile	Pro	Pro	Ser	Phe	Ala	Ser	Ile	Phe	Leu	Thr	Lys	Ser	Thr	Lys	Leu	370	375	380	
Thr	Cys	Leu	Val	Thr	Asp	Leu	Thr	Thr	Tyr	Asp	Ser	Val	Thr	Ile	Ser	385	390	395	400
Trp	Thr	Arg	Gln	Asn	Gly	Glu	Ala	Val	Lys	Thr	His	Thr	Asn	Ile	Ser	405	410	415	
Glu	Ser	His	Pro	Asn	Ala	Thr	Phe	Ser	Ala	Val	Gly	Glu	Ala	Ser	Ile	420	425	430	
Cys	Glu	Asp	Asp	Trp	Asn	Ser	Gly	Glu	Arg	Phe	Thr	Cys	Thr	Val	Thr	435	440	445	
His	Thr	Asp	Leu	Pro	Ser	Pro	Leu	Lys	Gln	Thr	Ile	Ser	Arg	Pro	Lys	450	455	460	
Gly	Val	Ala	Leu	His	Arg	Pro	Asp	Val	Tyr	Leu	Leu	Pro	Pro	Ala	Arg	465	470	475	480
Glu	Gln	Leu	Asn	Leu	Arg	Glu	Ser	Ala	Thr	Ile	Thr	Cys	Leu	Val	Thr	485	490	495	
Gly	Phe	Ser	Pro	Ala	Asp	Val	Phe	Val	Gln	Trp	Met	Gln	Arg	Gly	Gln	500	505	510	
Pro	Leu	Ser	Pro	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met	Pro	Glu	Pro	515	520	525	



Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu  
530 535 540

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu  
545 550 555 560

Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly  
565 570 575

Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly  
580 585 590

Thr Cys Tyr  
595

<210> 21  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(726)

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser  
1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96  
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala  
20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144  
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser  
35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192  
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

aaa cca gga cag cct cct aag ttg ctc att tac tgg gca tct acc cgg 240  
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288  
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
85 90 95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336  
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
100 105 110

tac tgt cag caa tat tat act act ctt ccg ctc act ttc ggc gga ggg 384  
Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly  
115 120 125

acc aag gtg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc 432  
 Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile  
 130 135 140

ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg 480  
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val  
 145 150 155 160

tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag 528  
 Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys  
 165 170 175

gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag 576  
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu  
 180 185 190

cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg 624  
 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu  
 195 200 205

agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc 672  
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 210 215 220

cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag 720  
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu  
 225 230 235 240

tgt tag 726  
 Cys

<210> 22  
 <211> 241  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser  
 1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala  
 20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser  
 35 40 45

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
 100 105 110  
 Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly  
 115 120 125  
 Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile  
 130 135 140  
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val  
 145 150 155 160  
 Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys  
 165 170 175  
 Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu  
 180 185 190  
 Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu  
 195 200 205  
 Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr  
 210 215 220  
 His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu  
 225 230 235 240

Cys

<210> 23  
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<400> 23  
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24

<210> 24  
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<400> 24  
 agcataatta aagccaagga ggag

24

<210> 25  
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 <212> DNA  
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<220>  
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<400> 25  
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 aattaagg 68

<210> 26  
 <211> 76  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized sequence

<400> 26  
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 ttcgatgatca ggccgg 76

<210> 27  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 27  
 gaggaattcc accatgaaga acc 23

<210> 28  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 28  
 gaggcggccg cttagtcagg atagcag 27

<210> 29  
 <211> 32  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 29  
 aaaagcggcc gcgatcataa tcagccatac ca 32

<210> 30  
 <211> 36  
 <212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 30

aaaactcgag aagcttagac atgataagat acattg

36

<210> 31

<211> 12

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized linker sequence

<400> 31

cccggatccg gg

12